the CLSI revised the clinical breakpoints for the azoles and the echinocandins against *Candida* species. Our objective was to evaluate what effect the new antifungal clinical breakpoints may have on antifungal susceptibility patterns in *Candida* species isolated from patients with candidemia in our geographic.
Methods: We performed a retrospective, descriptive analysis of triazole and echinocandin MICs against *Candida* species obtained from blood culture in one medical center of Southern Taiwan between January 2007 and January 2012. Antifungal susceptibility tests were determined using the broth microdilution method with Sensititre Yeast One system. Differences in susceptibility rates between the previous and revised breakpoints were assessed for significance by Fisher's exact test and a P value of <0.05 was considered significant.
Results: During the study period, 709 Candida isolates were obtained from the patients with candidemia. Isolates were classified as susceptibility based on both the previous and the recently revised CLSI clinical breakpoints. The significant reducing susceptibility in two azoles (fluconazole, voriconazole) and three echinocandins (anidulafungin, capsofungin, micafungin) against *C. tropicalis*, two echinocandins (anidulafungin, capsofungin) against *C. glabrata* and capsofungin against *C. krusei* were found.
Conclusions: The non-susceptible rates of azoles and echinocandin against some *Candida* species increase with interpretation according to the revised CLSI breakpoints. Further studies are needed to confirm the clinical relevance.

PS 2-363

CHANGES IN THE ENVIRONMENT CLEAN PROCESSES TO REDUCE ENVIRONMENTAL CLEAN COLONIZATION

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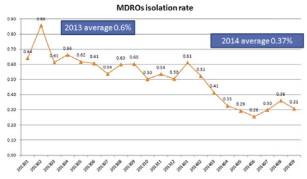
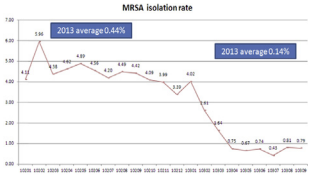
Purpose: Sanitation is important to the reduction of nosocomial infection. Our hospital adopted a color coding scheme for washcloths in 2009, but its success was limited. Therefore, in 2014 we adopted a series of changes in the sanitation procedures in order to reduce the incidence of multi-drug resistant microorganisms and healthcare-associated infections.
Methods: These changes include: 1) the establishment of a dedicated group of individuals who perform terminal cleaning of patients who were infected with multi-drug resistant organisms; 2) use of NaDCC disinfectant; 3) simplification of the procedure to make disinfectant; 4) avoiding repeated use of washcloths; 5) use of a log to document cleaning; 6) education and training of staff.
Results: Since 2014, the incidence of multi-drug resistant bacterial infections in our hospital declined from 0.6% to 0.37% (at a rate of 38.3%). In particular, the incidence of ORSA decreased from 0.44% to 0.14% (at a rate of 69.1%).





Conclusion: The Taiwan CDC began to promote a plan for antibiotic stewardship to decrease unnecessary antibiotic use, improve isolation procedures and hand hygiene. Actually, providing a clean environment for our hospitalized patients should also be a major part of patient safety and infection prevention.

PS 2-364

SURVEY FOR SAFE INJECTION IN A HOSPITAL IN KOREA

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Purpose: Guideline for safe injection has been recommended by the authorized institutions in the world such as WHO, CDC, and APIC. However, compliance about the recommendation for safe injection has not been known in Korea. The survey about safe injection was done to know the current status about safety of injection in a single university hospital in Korea.
Methods: Questionnaire was prepared based on the recommendation for injection safety. Paper survey was done for nurses and residents in the hospital about injection safety based on the recommendations by WHO and CDC.
Results: Three-hundred thirty-eight hospital staffs answered the survey (Overall response rate: 37.8% , 338/894). Drugs were prepared at unclean zone, such as, dressing cart (14.6%, 35/253) or even patient's area (13.8%, 37/253) against the recommendation for clean preparation. Thirty percent of the responders answered syringes or needles were not changed during the preparation of drugs and mixture of fluids for another patient. Drug-filled syringe was re-administered for the same patient (12.4%, 40/322). Large sized fluid bags were frequently used for drug mixture (29.5%, 83/281). Delayed administration of the prepared drugs was frequently experienced (35.5%, 91/256). Antimicrobial vial for single usage was reused for the same patient (14.3%, 36/293) or even multiple patients (2.0%, 6/293).
Conclusions: We need to enhance the knowledge about safe injection. Factors related with non-compliance should be identified from the point of prescription to administration for enhancement of compliance.

PS 2-366

THE WHOLE-GENOME SEQUENCING OF A ST 2196 *STAPHYLOCOCCUS AUREUS* BLOODSTREAM ISOLATE CAUSING METASTATIC INFECTION IN SOUTHERN TAIWAN

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Purpose: Metastatic infection is one of the most important complications of *Staphylococcus aureus* bacteremia (SAB). Nevertheless, the epidemiological studies of SAB patients with metastatic infection in Southern Taiwan are rare. According to our preliminary data, ST 2196 is a novel MLST type. The aim of this study was to investigate the novel ST 2196 SAB isolate with metastatic infection.
Methods: Metastatic infection was defined as patient had at least two different infection foci. The infection foci were defined as any of the following: infective endocarditis, mycotic aneurysm, osteomyelitis, septic arthritis, pyomyositis, necrotizing pneumonia or empyema, and abscess formation in any deep organ, such as liver or kidney. Modified Duke's criteria were applied for infective endocarditis. Necrotizing pneumonia was diagnosed according to clinical and radiological findings of a single or multiple cavitary lesions demonstrated in chest radiographs or chest CT scans. Multi-locus sequence typing (MLST) was performed. ST 2196 SAB isolate was analyzed by whole-genome sequencing with Illumina HiSeq 2000 sequencing platform.
Results: Based on the assemble result of ST 2196 SAB isolate, we found that the genome size was 2,810,148 bp, GC content was 32.32%, the number of scaffold was 32, and the number of contig was 133. Comparing with reference strain MSHR1132, we found that ST 2196 SAB isolate contains 17,772 SNPs including 9,200 synonymous mutations and 4,303 non-synonymous mutations. Comparing with ARDB-Antibiotic Resistance Genes Database, we found some antibiotic resistance genes which might contribute to resistant in bacitracin, fosfomycin, tigecycline and norfloxacin in the chromosome.
Conclusions: To our best knowledge, this is first report of the novel ST 2196 SAB isolate with metastatic infection in the world. Clinicians should more carefully treat patients with SAB and metastatic infection.